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DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 18.7 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC018048; AAI18048.1;
DR PRINTS: PRO1641; PROMCHFAMILY.
KW Hypothetical protein.
SQ SEQUENCE 165 AA; 18679 MW; 2339E8938BEC499 CRC64;

Query Match 100.0%; Score 90; DB 11; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.8e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 LRCMLGRVYRRCMOV 15
Db 151 LRCMLGRVYRRCMOV 165

RESULT 3
09D20
ID 09D20 PRELIMINARY; PRT: 165 AA.
AC 09D20;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE A230109K23R1K protein.
GN A230109K23R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=HYPOPHALAMUS;
RA MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shingawa A., Shideta K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staudt F., Suzuki K., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,
RA Guelinich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima M., Mazzarelli J., Mombarts P.,
RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Sessa T., Shideta Y., Storch K.F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK020723; BAB32189.1;
DR MGD: MGI:1925014; A230109K23R1K.
DR PRINTS: PRO1641; PROMCHFAMILY.
SQ SEQUENCE 165 AA; 18516 MW; 1872B6BD4BEEAC2 CRC64;
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QY 1 LRCMLGRVYRRCMOV 15
Db 151 LRCMLGRVYRRCMOV 165

RESULT 4
09I9L6
ID 09I9L6 PRELIMINARY; PRT: 150 AA.
AC 09I9L6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Melanin-concentrating hormone-like protein.
OS Paratichthys olivacea (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorphi; Pleuronectiformes;
OC Pleuronectoidae; Paratichthyidae; Paratichthys.
OX NCBI_TaxID=8255;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Jeon J., Lee J., Song Y.;
RT "Melanin-concentrating hormone-like protein.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF236090; AAF67166.1;
DR PRINTS: PRO1641; PROMCHFAMILY.
SQ SEQUENCE 150 AA; 16913 MW; 117A280F46ED4499 CRC64;

Query Match 90.0%; Score 81; DB 13; Length 150;
Best Local Similarity 85.7%; Pred. No. 2.5e-06;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRCMLGRVYRRCMOV 14
Db 132 LRCMLGRVYRRCMOV 145

RESULT 5
09B0D1
ID 09B0D1 PRELIMINARY; PRT: 86 AA.
AC 09B0D1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Pro-melanin-concentrating hormone-like 2 protein.
GN PCHL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RA MEDLINE-21108351; PubMed-1181993;
RA Courseaux A., Nahon J.L.;
RT "Birth of two chimeric genes in the Homiidae lineage.";
RL Science 291:1293-1297(2001).
DR EMBL: AY008413; AAK31297.1;
DR EMBL: AY008420; AAK31290.1;
DR EMBL: AY008412; AAK31296.1;
DR PRINTS: PRO1641; PROMCHFAMILY.
SQ SEQUENCE 86 AA; 9856 MW; 1C8D698786847471 CRC64;

Query Match 85.6%; Score 77; DB 4; Length 86;
Best Local Similarity 86.7%; Pred. No. 7.2e-06;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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RESULT 6

09B010 PRELIMINARY; PRT; 86 AA.
 ID 09B010
 AC 09B010; (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DE Pro-melanin-concentrating hormone-like 1 protein.
 GN PCHL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RX MEDLINE=21108351; PubMed=11181993;
 RA Courseaux A., Nahon J.L.;
 RT "Birth of two chimeric genes in the Hominiidae lineage."
 RL Science 291:1293-1297(2001).
 DR EMBL; AY008411; AKS1295.1; -;
 DR EMBL; AY028318; AKS1289.1; -;
 DR PRINTS; PR01641; PROMCHFAMILY.
 SQ SEQUENCE 86 AA; 9715 MW; BC5EC470EDA8F7F3 CRC64;

Query Match 80.0%; Score 72; DB 4; Length 86;
 Best Local Similarity 80.0%; Pred. No. 5.2e-05;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LRCMLGRVTRPCMOV 15
 DB 72 LSCMLGRVTRPCMOV 86

RESULT 7

088259 PRELIMINARY; PRT; 85 AA.
 ID 088259
 AC 088259; (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DE Mszf54 (Fragment).
 GN Mszf54.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL6;
 RX MEDLINE=98296253; PubMed=9630514;
 RA Agata Y., Matsuda E., Shimizu A.;
 RT "Rapid and efficient cloning of cDNAs encoding Krueppel-like zinc
 RT finger proteins by degenerate PCR."
 RL Gene 213:55-64(1998)
 DR EMBL; AB010364; BAB31420.1; -;
 DR HSRP; P08048; ZNF;
 DR InterPro; IPR000822; Znf_C2H2.
 DR Pfam; PF00906; Zf-C2H2; 3.
 DR SMART; SM00355; ZNF_C2H2; 3.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
 KW DNA-binding; Metal-binding; Zinc-finger.
 FT NON-TER 1
 SQ SEQUENCE 85 AA; 10007 MW; F0FA94C459DBEDA CRC64;

Query Match 50.6%; Score 45.5; DB 11; Length 85;
 Best Local Similarity 46.7%; Pred. No. 1.8;
 Matches 7; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

OY 2 RC-MLGRVTRPCMOV 15
 DB 1 RC-MLGRVTRPCMOV 15

DB 33 KCEVGRVTRPCMOV 47

RESULT 8

08X2X6 PRELIMINARY; PRT; 186 AA.
 ID 08X2X6
 AC 08X2X6; (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DE Hypothetical protein ECS4988.
 GN ECS4988.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Mureta T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasekawa C., Ogawara N., Yasunaga T.,
 RA Kubara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12."
 RL DNA Res. 8:11-22(2001).
 DR EMBL; AP002567; BAB38411.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 186 AA; 21454 MW; C5EDE1E6BCA989 CRC64;

Query Match 49.4%; Score 44.5; DB 16; Length 186;
 Best Local Similarity 57.1%; Pred. No. 5.8;
 Matches 8; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY 1 LRCMLGRVTRPCMOV 14
 DB 159 LECILNR-YKPAWQ 171

RESULT 9

09D3R4 PRELIMINARY; PRT; 154 AA.
 ID 09D3R4
 AC 09D3R4; (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DE 4933439J11R1K protein.
 GN 4933439J11R1K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TESTIS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto N.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirini L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderrelli R., Barsh G.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Goncalves M.F.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombert P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Wetz C., Whitlaker C., Wilming L.,

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB072778; BAB69747.1;
 KW Hypothetical protein.
 SQ SEQUENCE 103 AA; 11326 MW; D8547BDDA141195 CRC64;

Query Match 46.7%; Score 42; DB 6; Length 103;
 Best Local Similarity 46.2%; Pred. No. 8.8;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 3 CMLGRVYRPMQOV 15
 DB 52 CDLGILSNPCWRL 64

RESULT 13

P71972 PRELIMINARY; PRT; 250 AA.
 AC P71972;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein RV2675c.
 GN RV2675C OR MTCY441.44C OR MT2749.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekela F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feldwell T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborn J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skellern S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CDC 1551 / OSHKOSH;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Helt D., Hickey E.,
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;

RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: STRONG. IN C-TERMINAL REGION TO M.LEPRAE U1764Z.
 DR EMBL: Z80225; CAB0328.1;
 DR EMBL: AE007105; AKK47064.1;
 DR TIGR: MT2749;
 DR Tuberculin: RV2675c;
 DR InterPro: IPR000051; SAM_bind.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 250 AA; 27545 MW; 2EC9718C7550F32C CRC64;

Query Match 46.7%; Score 42; DB 16; Length 250;
 Best Local Similarity 33.3%; Pred. No. 21;
 Matches 9; Conservative 4; Mismatches 2; Indels 12; Gaps 1;

OY 1 LRCML-----GRVYRPMQOV 15
 DB 218 VRCVLEFRRAIKPWLVGSRVHAPMEV 244

RESULT 14

ID 09GS12 PRELIMINARY; PRT; 311 AA.
 AC 09GS12;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE F56H6.13 protein.
 GN F56H6.13.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kershaw J.K.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RT Science 282:2012-2018(1998).
 DR EMBL: Z81553; CAC14353.1;
 SQ SEQUENCE 311 AA; 36614 MW; 4A9960CE41C1027B CRC64;

Query Match 46.7%; Score 42; DB 5; Length 311;
 Best Local Similarity 33.3%; Pred. No. 25;
 Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 LRCMLGRVYRPMQOV 15
 DB 155 MRCVRRITNGIMINT 169

RESULT 15
 ID 091HR4 PRELIMINARY; PRT; 555 AA.
 AC 091HR4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Glycoprotein E (Fragment).
 OS Pseudorabies virus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 OX NCBI_TaxID=10345;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GDANGONG;
 RA Lou G.M.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF403050; AAK95640.1;
 DR InterPro: IPR003404; Herpes-glycopE.
 DR Pfam: PF02480; Herpes_gE; 1.
 FT NON_TER 1
 FT NON_TER 555
 FT NON_TER 555
 SQ SEQUENCE 555 AA; 59871 MW; 79CBEF2F03003CDB CRC64;

Query Match 46.7%; Score 42; DB 12; Length 555;
 Best Local Similarity 63.6%; Pred. No. 44;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 RCMGRVYRPMQOV 12
 DB 252 RCLLYVYRPMQOV 262

Search completed: June 25, 2003, 11:54:03
 Job time : 37.6 secs